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<110> OXAGEN LIMITED
Jonathon M. TINSLEY

<120> Ligand

<130> 117-585 / N.89652C GCW

<140> US

<141> 2006-05-15

<150> PCT/GB2004/005057

<151> 2004-12-02

<150> GB 0328275.3

<151> 2003-12-05

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<151> 2004-02-11

<150> GB 0418568.2

<151> 2004-08-19

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cca gag gat gaa tat gat gtc ctc ata gaa ggt gaa ctg gag agc gat 152
Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp
20 25 30 35

gag gca gag caa tgt gac aag tat gac gcc cag gca ctc tca gcc cag 200
Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu Ser Ala Gln
40 45 50

ctg gtg cca tca ctc tgc tct gct gtg ttt gtg atc ggt gtc ctg gac 248
Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp
55 60 65

aat ctc ctg gtt gtg ctt atc ctg gta aaa tat aaa gga ctc aaa cgc Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg 70 75 80	296
gtg gaa aat atc tat ctt cta aac ttg gca gtt tct aac ttg tgt ttc Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn Leu Cys Phe 85 90 95	344
ttg ctt acc ctg ccc ttc tgg gct cat gct ggg ggc gat ccc atg tgt Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp Pro Met Cys 100 105 110 115	392
aaa att ctc att gga ctg tac ttc gtg ggc ctg tac agt gag aca ttt Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser Glu Thr Phe 120 125 130	440
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ggc aac ttt ttc tca gcc agg agg agg gtg ccc tgt ggc atc att aca Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly Ile Ile Thr 150 155 160	536
agt gtc ctg gca tgg gta aca gcc att ctg gcc act ttg cct gaa tac Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu Pro Glu Tyr 165 170 175	584
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aaa gaa cac ttc tcc ctg agt gac tgc aag agc agc tac aat ctg gac Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr Asn Leu Asp 280 285 290	920

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 Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His Cys Cys Ile
 295 300 305

 aac cct ctc ctg tat gcg ttt ctt gat ggg aca ttt agc aaa tac ctc 1016
 Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu
 310 315 320

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 Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln Pro Arg Gly
 325 330 335

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 Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu
 340 345 350 355

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 Val

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 Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly
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 Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly
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Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn
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 Leu Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp
 100 105 110
 Pro Met Cys Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser
 115 120 125
 Glu Thr Phe Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe
 130 135 140
 Leu His Lys Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly
 145 150 155 160
 Ile Ile Thr Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu
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 Pro Glu Tyr Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys
 180 185 190
 Cys Ala Phe Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp
 195 200 205
 Lys His Phe Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro
 210 215 220
 Leu Phe Ile Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg
 225 230 235 240
 Phe Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Ile Met
 245 250 255
 Val Val Phe Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu
 260 265 270
 Ser Thr Phe Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr
 275 280 285
 Asn Leu Asp Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His
 290 295 300
 Cys Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser
 305 310 315 320
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gtggttttctc gtgccctca gggtcaggag cagtctgacg aaaaggaggg catccactgt      240
ccgggggccat tcccacagct cccggatgct gggctctggag gctgcgccct tcccctgcag      300
gagctcagcc cagtgggcag tctgaag atg gcc aat tac acg ctg gca cca gag      354
                               Met Ala Asn Tyr Thr Leu Ala Pro Glu
                               1                               5

gat gaa tat gat gtc ctc ata gaa ggt gaa ctg gag agc gat gag gca      402
Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp Glu Ala
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gag caa tgt gac aag tat gac gcc cag gca ctc tca gcc cag ctg gtg      450
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cca tca ctc tgc tct gct gtg ttt gtg atc ggt gtc ctg gac aat ctc      498
Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp Asn Leu
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ctg gtt gtg ctt atc ctg gta aaa tat aaa gga ctc aaa cgc gtg gaa      546
Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg Val Glu
60                               65                               70

aat atc tat ctt cta aac ttg gca gtt tct aac ttg tgt ttc ttg ctt      594
Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn Leu Cys Phe Leu Leu
75                               80                               85

acc ctg ccc ttc tgg gct cat gct ggg ggc gat ccc atg tgt aaa att      642
Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp Pro Met Cys Lys Ile
90                               95                               100                               105

ctc att gga ctg tac ttc gtg ggc ctg tac agt gag aca ttt ttc aat      690
Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser Glu Thr Phe Phe Asn
110                               115                               120

tgc ctt ctg act gtg caa agg tac cta gtg ttt ttg cac aag ggc aac      738
Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe Leu His Lys Gly Asn
125                               130                               135

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Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu Pro Glu Tyr Val Val	
155 160 165	
tat aaa cct cag atg gaa gac cag aaa tac aag tgt gca ttt agc aga	882
Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys Cys Ala Phe Ser Arg	
170 175 180 185	
act ccc ttc ctg cca gct gat gag aca ttc tgg aag cat ttt ctg act	930
Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp Lys His Phe Leu Thr	
190 195 200	
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Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro Leu Phe Ile Phe Thr	
205 210 215	
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Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg Phe Arg Glu Gln Arg	
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tat agc ctt ttc aag ctt gtt ttt gcc ata atg gta gtc ttc ctt ctg	1074
Tyr Ser Leu Phe Lys Leu Val Phe Ala Ile Met Val Val Phe Leu Leu	
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Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu Ser Thr Phe Lys Glu	
250 255 260 265	
cac ttc tcc ctg agt gac tgc aag agc agc tac aat ctg gac aaa agt	1170
His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr Asn Leu Asp Lys Ser	
270 275 280	
gtt cac atc act aaa ctc atc gcc acc acc cac tgc tgc atc aac cct	1218
Val His Ile Thr Lys Leu Ile Ala Thr Thr His Cys Cys Ile Asn Pro	
285 290 295	
ctc ctg tat gcg ttt ctt gat ggg aca ttt agc aaa tac ctc tgc cgc	1266
Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu Cys Arg	
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Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln Pro Arg Gly Gln Ser	
315 320 325	
gca caa ggc aca tcg agg gaa gaa cct gac cat tcc acc gaa gtg taa	1362
Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu Val	
330 335 340	
actagcatcc accaaatgca agaagaataa acatggattt tcatctttct gcattatttc	1422
atgtaaatctt tctacacatt tgtatacaaaa atcgataca ggaagaaaag ggagaggtga	1482
gctaacattt gctaagcact gaatttgtct caggcaccgt gcaaggctct ttacaaacgt	1542

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Ala	Gln	Ala	Leu	Ser	Ala	Gln	Leu	Val	Pro	Ser	Leu	Cys	Ser	Ala	Val	35	40	45	
Phe	Val	Ile	Gly	Val	Leu	Asp	Asn	Leu	Leu	Val	Val	Leu	Ile	Leu	Val	50	55	60	
Lys	Tyr	Lys	Gly	Leu	Lys	Arg	Val	Glu	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	65	70	75	80
Ala	Val	Ser	Asn	Leu	Cys	Phe	Leu	Leu	Thr	Leu	Pro	Phe	Trp	Ala	His	85	90	95	
Ala	Gly	Gly	Asp	Pro	Met	Cys	Lys	Ile	Leu	Ile	Gly	Leu	Tyr	Phe	Val	100	105	110	
Gly	Leu	Tyr	Ser	Glu	Thr	Phe	Phe	Asn	Cys	Leu	Leu	Thr	Val	Gln	Arg	115	120	125	
Tyr	Leu	Val	Phe	Leu	His	Lys	Gly	Asn	Phe	Phe	Ser	Ala	Arg	Arg	Arg	130	135	140	
Val	Pro	Cys	Gly	Ile	Ile	Thr	Ser	Val	Leu	Ala	Trp	Val	Thr	Ala	Ile	145	150	155	160
Leu	Ala	Thr	Leu	Pro	Glu	Tyr	Val	Val	Tyr	Lys	Pro	Gln	Met	Glu	Asp	165	170	175	
Gln	Lys	Tyr	Lys	Cys	Ala	Phe	Ser	Arg	Thr	Pro	Phe	Leu	Pro	Ala	Asp	180	185	190	
Glu	Thr	Phe	Trp	Lys	His	Phe	Leu	Thr	Leu	Lys	Met	Asn	Ile	Ser	Val	195	200	205	

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 Lys Thr Leu Arg Phe Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val
 225 230 235 240
 Phe Ala Ile Met Val Val Phe Leu Leu Met Trp Ala Pro Tyr Asn Ile
 245 250 255
 Ala Phe Phe Leu Ser Thr Phe Lys Glu His Phe Ser Leu Ser Asp Cys
 260 265 270
 Lys Ser Ser Tyr Asn Leu Asp Lys Ser Val His Ile Thr Lys Leu Ile
 275 280 285
 Ala Thr Thr His Cys Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Asp
 290 295 300
 Gly Thr Phe Ser Lys Tyr Leu Cys Arg Cys Phe His Leu Arg Ser Asn
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 ctc tgc tcc tgt gca caa gtt ggt acc aac aaa gag ctc tgc tgc ctc 156
 Leu Cys Ser Cys Ala Gln Val Gly Thr Asn Lys Glu Leu Cys Cys Leu
 20 25 30

 gtc tat acc tcc tgg cag att cca caa aag ttc ata gtt gac tat tct 204
 Val Tyr Thr Ser Trp Gln Ile Pro Gln Lys Phe Ile Val Asp Tyr Ser
 35 40 45

 gaa acc agc ccc cag tgc ccc aag cca ggt gtc atc ctc cta acc aag 252
 Glu Thr Ser Pro Gln Cys Pro Lys Pro Gly Val Ile Leu Leu Thr Lys
 50 55 60

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Arg Gly Arg Gln Ile Cys Ala Asp Pro Asn Lys Lys Trp Val Gln Lys
65              70              75              80

tac atc agc gac ctg aag ctg aat gcc tga ggggcctgga agctgcgagg      350
Tyr Ile Ser Asp Leu Lys Leu Asn Ala
85

gcccagtga cttggtgggc ccaggaggga acaggagcct gagccagggc aatggccctg      410
ccaccctgga ggccacctct tctaagagtc ccatctgcta tgcccagcca cattaactaa      470
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ttcccttcaa ctcttcgtac attcaatgca tggatcaatc agtgtgatta gctttctcag      650
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Val Tyr Thr Ser Trp Gln Ile Pro Gln Lys Phe Ile Val Asp Tyr Ser
35              40              45

Glu Thr Ser Pro Gln Cys Pro Lys Pro Gly Val Ile Leu Leu Thr Lys
50              55              60

Arg Gly Arg Gln Ile Cys Ala Asp Pro Asn Lys Lys Trp Val Gln Lys
65              70              75              80

Tyr Ile Ser Asp Leu Lys Leu Asn Ala
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